B. Amendment to the Claims

Please amend claims 1 and 2 and add new claim 9 as follows. A listing of all claims in the application is provided.

1. (Currently Amended) A method for identifying a base sequence present in a target single-stranded nucleic acid comprising the steps of:

(a) preparing a probe array in which single-stranded nucleic acid probes of No. 1 to No. n ($n \geq 2$) are arranged as isolated spots on a substrate;

(b) reacting a single-stranded nucleic acid, which has a base sequence fully complementary to a base sequence of one of the single-stranded nucleic acid probes and is fluorescence-labeled, with the probe array under such conditions that single-stranded nucleic acids complementary to each other form a double-stranded nucleic acid;

removing the unreacted labeled single-stranded nucleic acid; and

measuring fluorescence intensity of each spot of the probe array to obtain a first image template pattern showing a relationship between location of the probes and fluorescent characteristics;

(c) performing the same operation as the step (b) for each of remaining single-stranded nucleic acid probes using a second to a nth single-stranded nucleic acid, and obtaining image template patterns of No. 2 to No. n showing a relationship between location and fluorescent characteristics of the probes;

(d) performing the same operation as the step (b) using a sample containing the target single-stranded nucleic acid of the base sequence to obtain a sample pattern showing a relationship between a position and fluorescent characteristics; [[and]]

(e) comparing the sample pattern obtained in the step (d) with n pieces of said image template patterns obtained in the steps (b) and (c), to find a template pattern substantially identical to the sample pattern; and

(f) ~~identify a template pattern showing substantially the same pattern as the sample pattern and~~ identifying the base sequence of the single-stranded nucleic acid used for the preparation of the identified image template pattern as the base sequence of the target single-stranded nucleic acid.

2. (Currently Amended) A method for identifying a base sequence present in a target single-stranded nucleic acid comprising the steps of:

(a) preparing a probe array in which single-stranded nucleic acid probes of No. 1 to No. n ($n \geq 2$) are arranged as isolated spots on a substrate;

(b) reacting a single-stranded nucleic acid which has a base sequence fully complementary to a base sequence of one of the single-stranded nucleic acid probes and is fluorescence-labeled, with the probe array under such conditions that single-stranded nucleic acids complementary to each other form a double-stranded nucleic acid;

removing the unreacted labeled single-stranded nucleic acid; and

measuring fluorescence intensity of each spot of the probe array to obtain a first template pattern showing a relationship between location of the probes and fluorescent characteristics;

(c) analyzing the first template pattern to locate probes and to calculate a mean value of fluorescence intensities (Fi) of the double-stranded nucleic acids having i of mismatched base pairs, where i is an integer not less than 1;

(d) calculating a difference (F1, 0) between the fluorescence intensity of the fully complementary double-stranded nucleic acid without mismatch (F0) and the mean value of the fluorescence intensities of the double-stranded nucleic acids having one-base mismatch (F1), further calculating a difference (Fi+1, i) between a fluorescence intensity of a double-stranded nucleic acid having (i+1) base mismatches (Fi+1) and a fluorescence intensity of a double-stranded nucleic acid having i-base mismatches (Fi), and identifying i being $Fi+1, i << Fi, i-1$;

(e) preparing a second template pattern of positive probe spots of probes having base sequences differing from the base sequence of the second probe by i or less bases where i is determined in said step (d), wherein negative probe spots are probes having base sequences differing from the second probe by more than i bases;

(f) performing the same operation as the step (e) for each of remaining single-stranded nucleic acid probes and obtaining template patterns of No. 3 to No. n showing a relationship between location and fluorescent characteristics of the probes;

(g) performing the same operation as the step (b) using a sample containing the target single-stranded nucleic acid of the base sequence to obtain a sample pattern showing a relationship between a position and fluorescent characteristics; [[and]]

(h) comparing the sample pattern obtained in the step (g) with n pieces of template patterns obtained in the steps (b), (c) and (e), to find a template pattern substantially identical to the sample pattern; ~~identifying a template pattern showing essentially the same pattern as the sample pattern;~~ and

(i) determining the base sequence of the target single-stranded nucleic acid to be a base sequence complementary to the base sequence of the probe taken for the preparation of the identified template pattern.

3. (Original) The method according to claim 2, wherein the step (g) further comprises the substep of obtaining a two-valued pattern of the fluorescence intensity by using the threshold fluorescence intensity Fi.

4. (Original) The method according to claim 2, wherein the length of the probe is 8 mer to 30 mer.

5. (Original) The method according to claim 4, wherein the length of the probe is 12 mer to 25 mer.

6. (Original) The method according to claim 2, wherein the number of the mismatched base pairs (i) is 1.

7-8. (Cancelled).

9. (New) A method for identifying a mutation at a plurality of sites in a region in a target single-stranded nucleic acid comprising the steps of:

(a) preparing a probe array in which single-stranded nucleic acid probes of No. 1 to No. n ($n \geq 3$) are arranged as isolated spots on a substrate, where probes as a whole cover every mutation expected at the sites;

(b) reacting a single-stranded nucleic acid, which has a base sequence fully complementary to a base sequence of one of the single-stranded nucleic acid probes and is fluorescence-labeled, with the probe array under such conditions that single-stranded nucleic acids complementary to each other form a double-stranded nucleic acid;

removing the unreacted labeled single-stranded nucleic acid; and

measuring fluorescence intensity of each spot of the probe array to obtain a first image template pattern showing a relationship between location of the probes and fluorescent characteristics;

(c) performing the same operation as the step (b) for each of remaining single-stranded nucleic acid probes using a second to a nth single-stranded nucleic acid, and obtaining image template patterns of No. 2 to No. n showing a relationship between location and fluorescent characteristics of the probes;

(d) performing the same operation as the step (b) using a sample containing the target single-stranded nucleic acid of the base sequence to obtain a sample pattern showing a relationship between a position and fluorescent characteristics;

(e) comparing the sample pattern obtained in the step (d) with n pieces of said image template patterns obtained in the steps (b) and (c), to find a template pattern substantially identical to the sample pattern; and

(f) identifying the mutation in the target nucleic acid from the sequence of the single-stranded nucleic acid that produced the substantially identical template pattern.